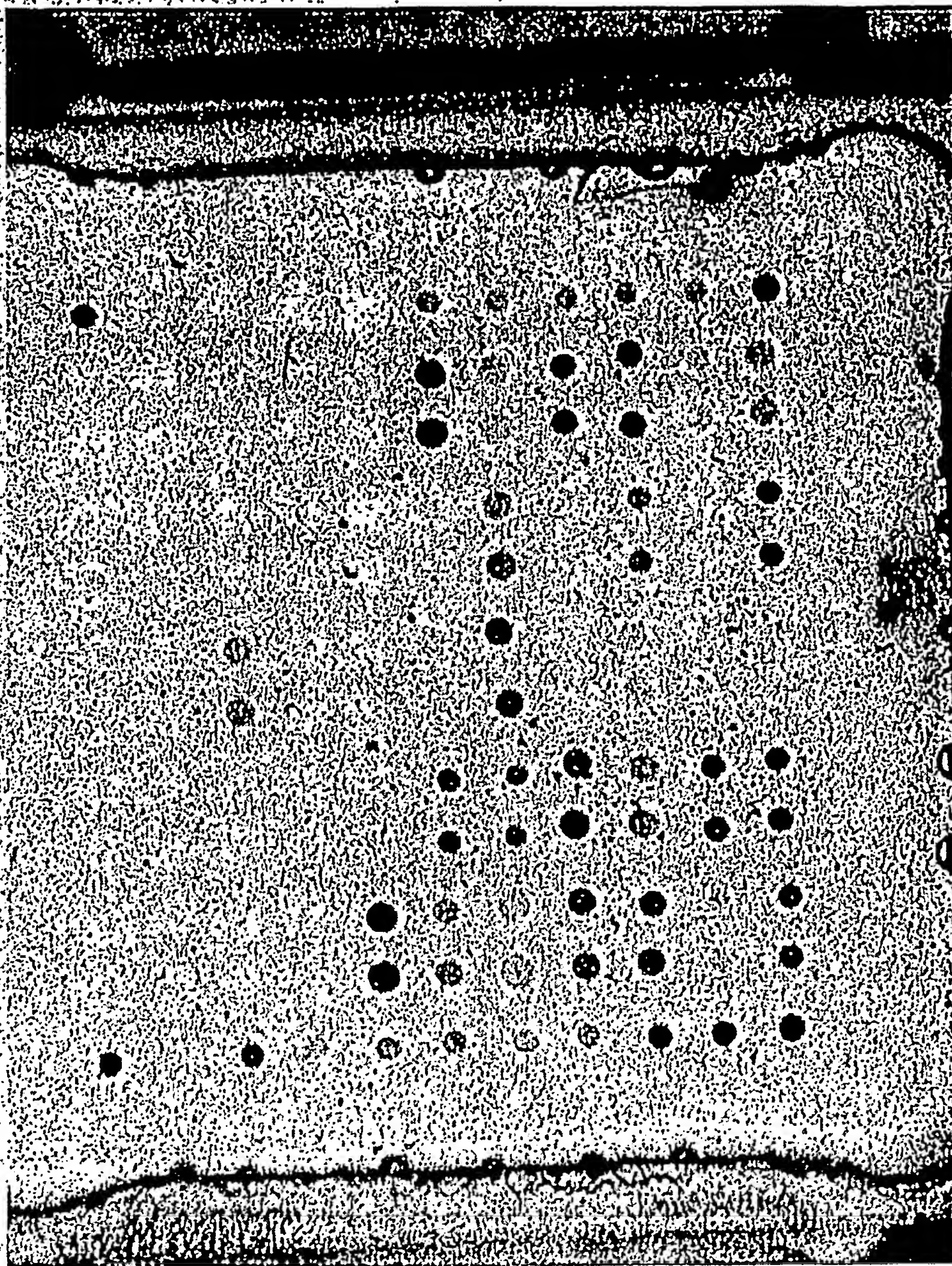


Fig.1

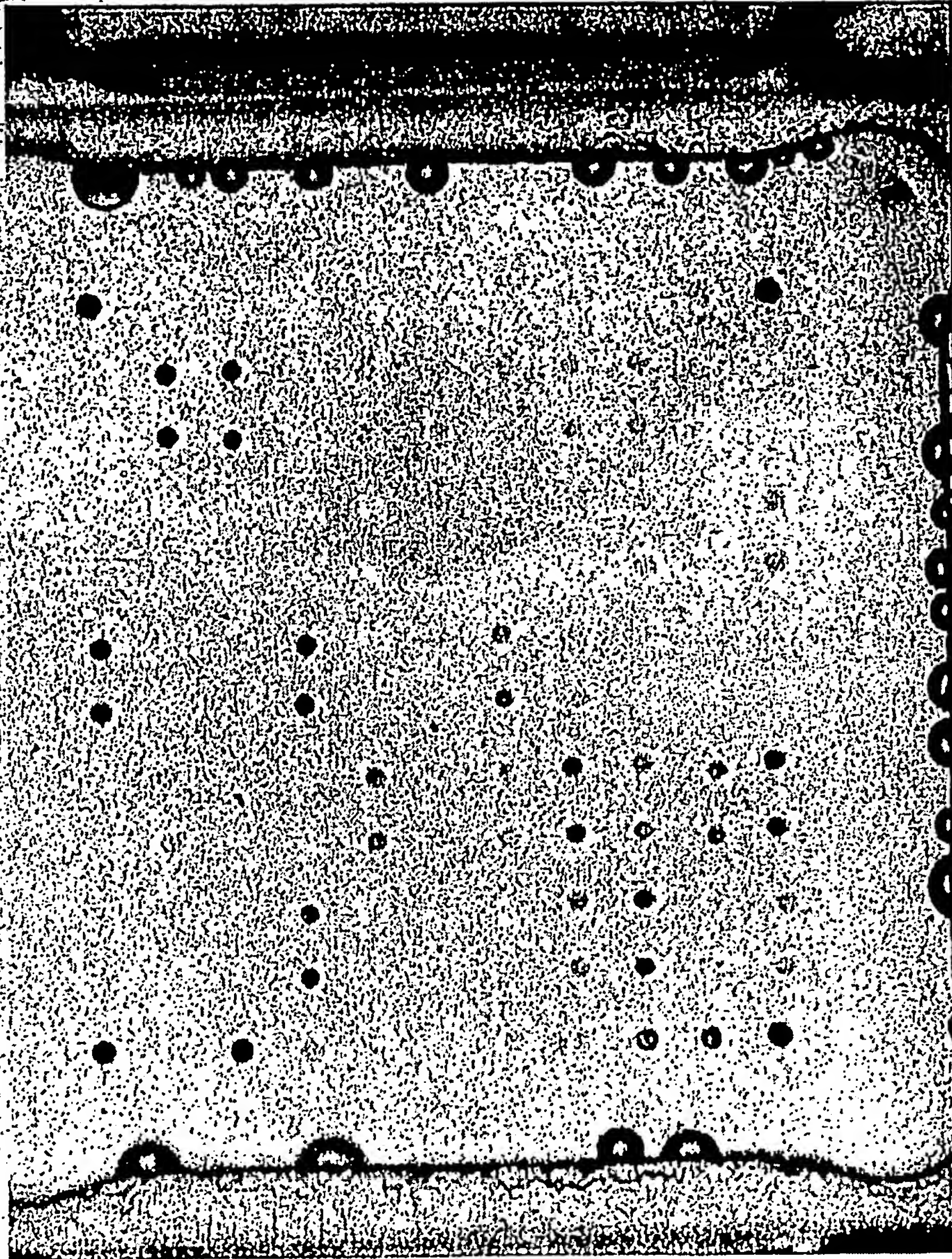
P. aeruginosa AT-Chip



ZW117

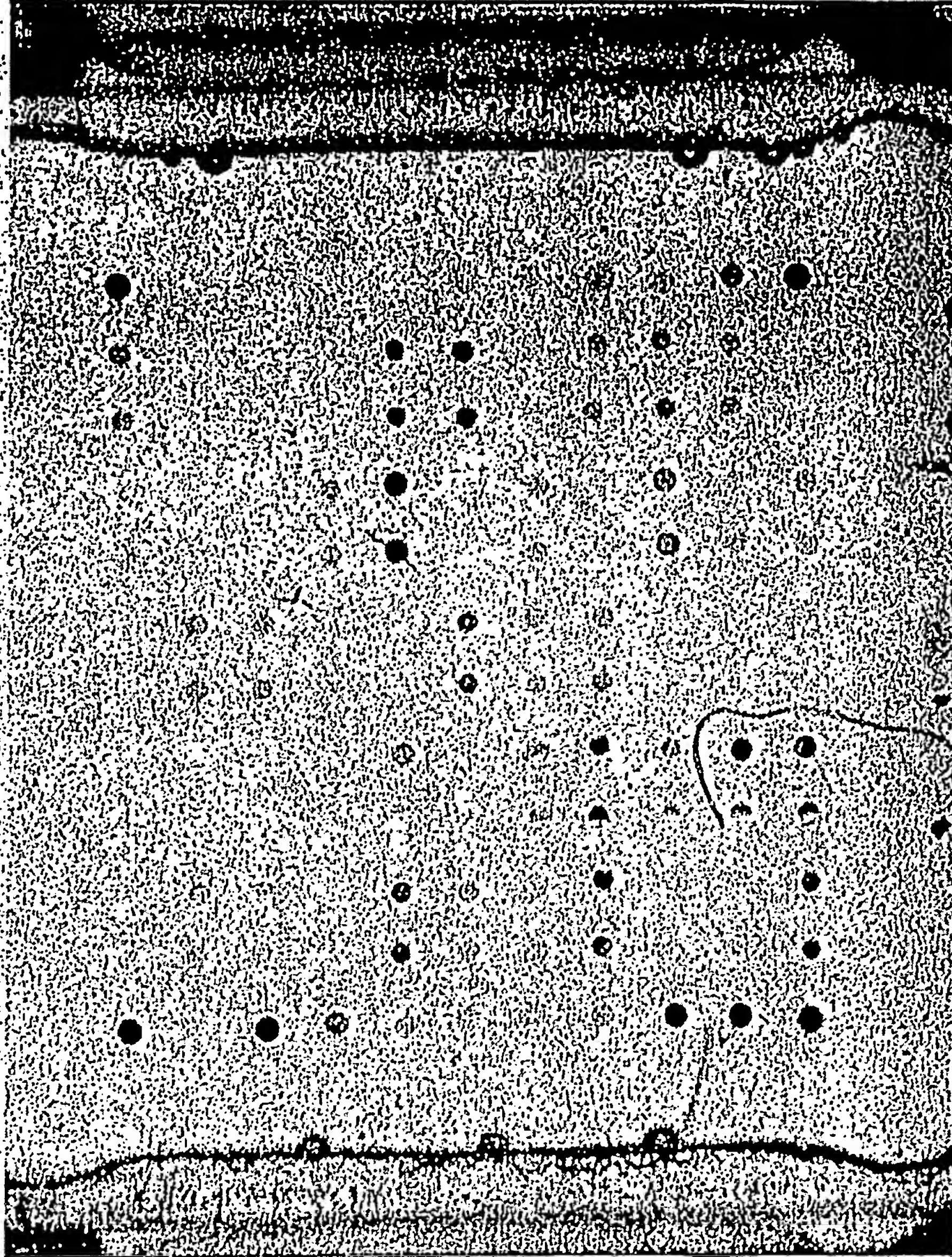
Fig.2

P. aeruginosa AT-Chip



RP17

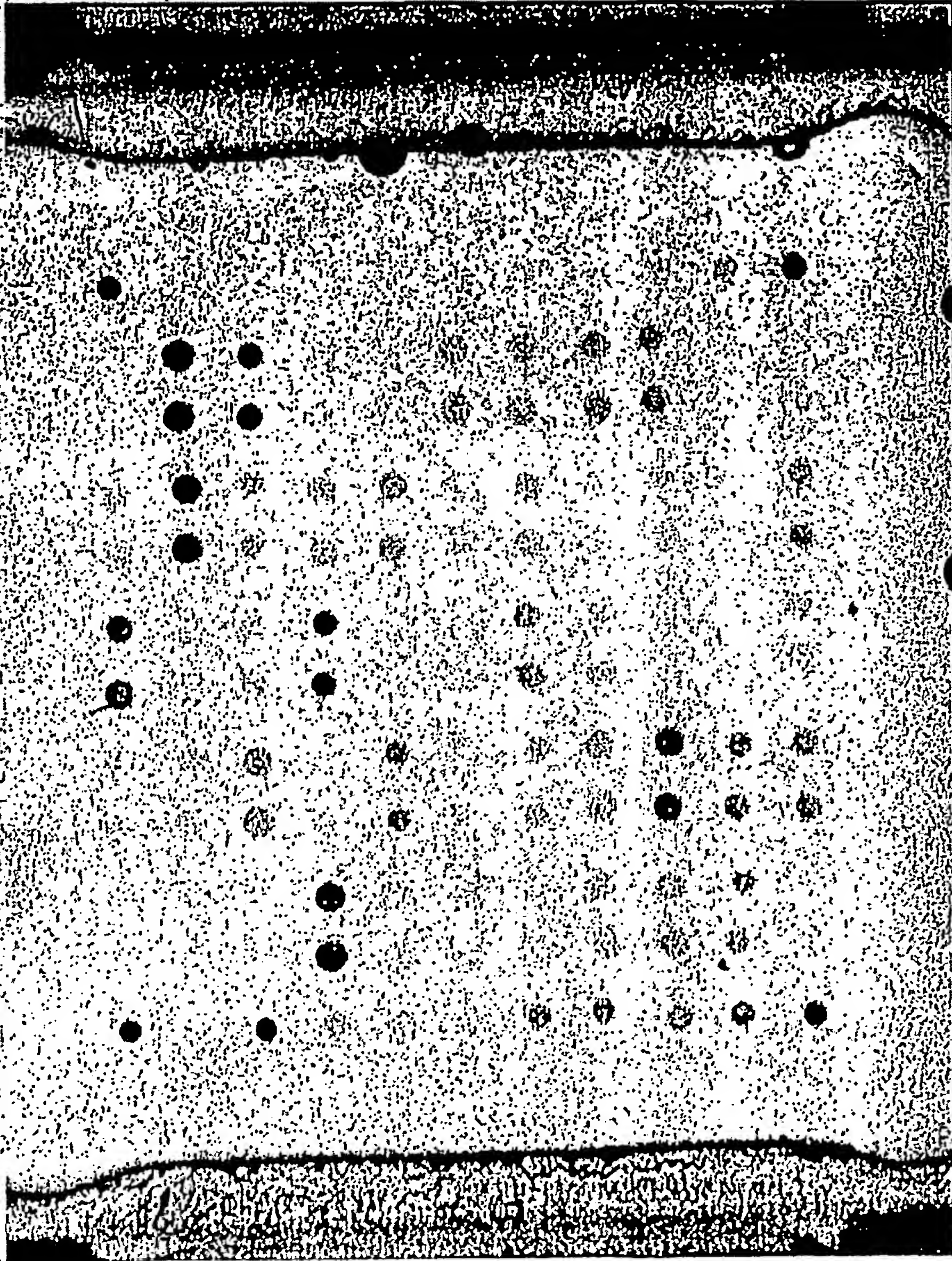
P. aeruginosa AT-Chip



TB

Fig.4

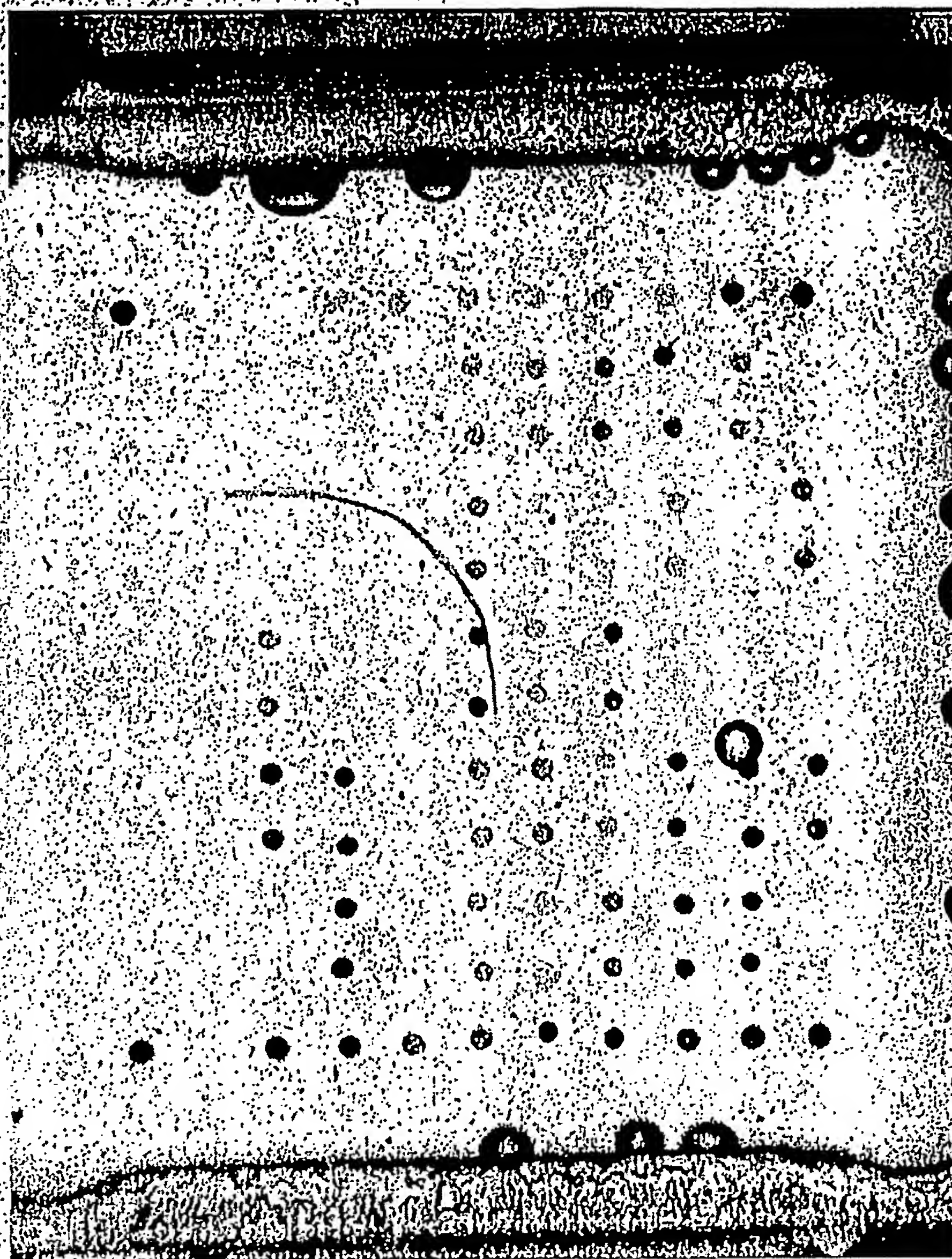
P. aeruginosa AT-Chip



SG17M

Fig.5

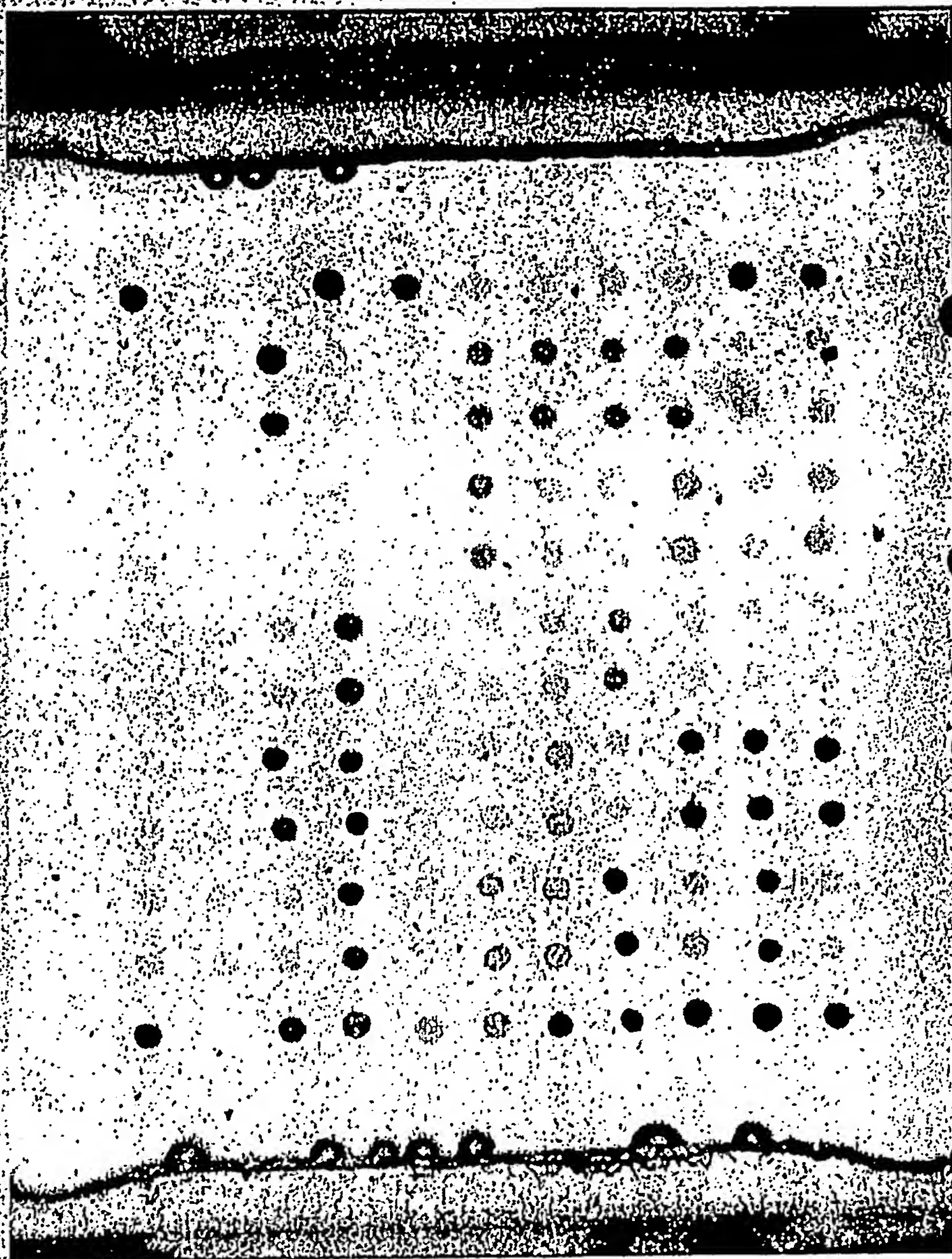
P. aeruginosa AT-Chip



BST85

Fig.6

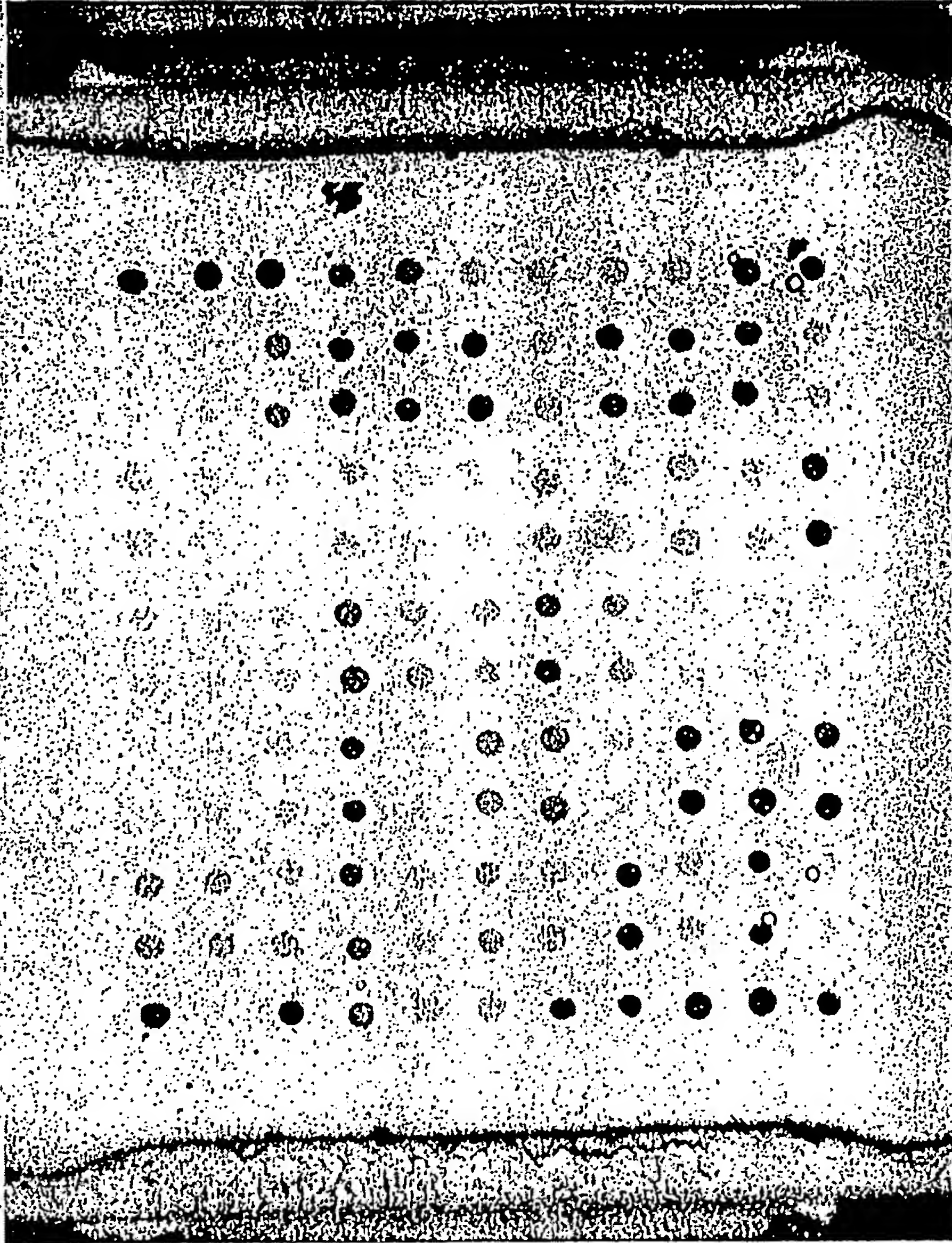
P. aeruginosa AT-Chip



AL5846

Fig.7

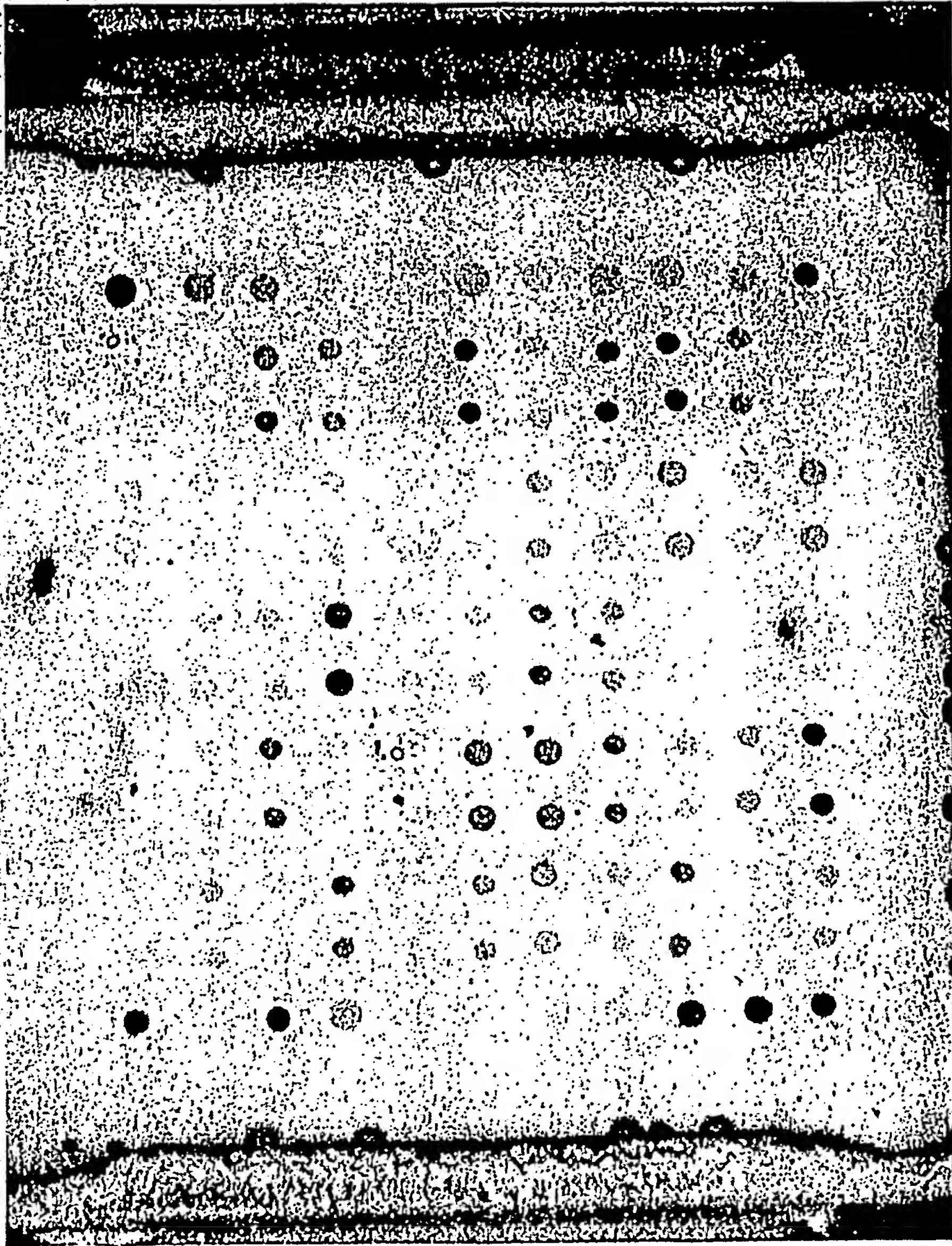
P. aeruginosa AT-Chip



PT12

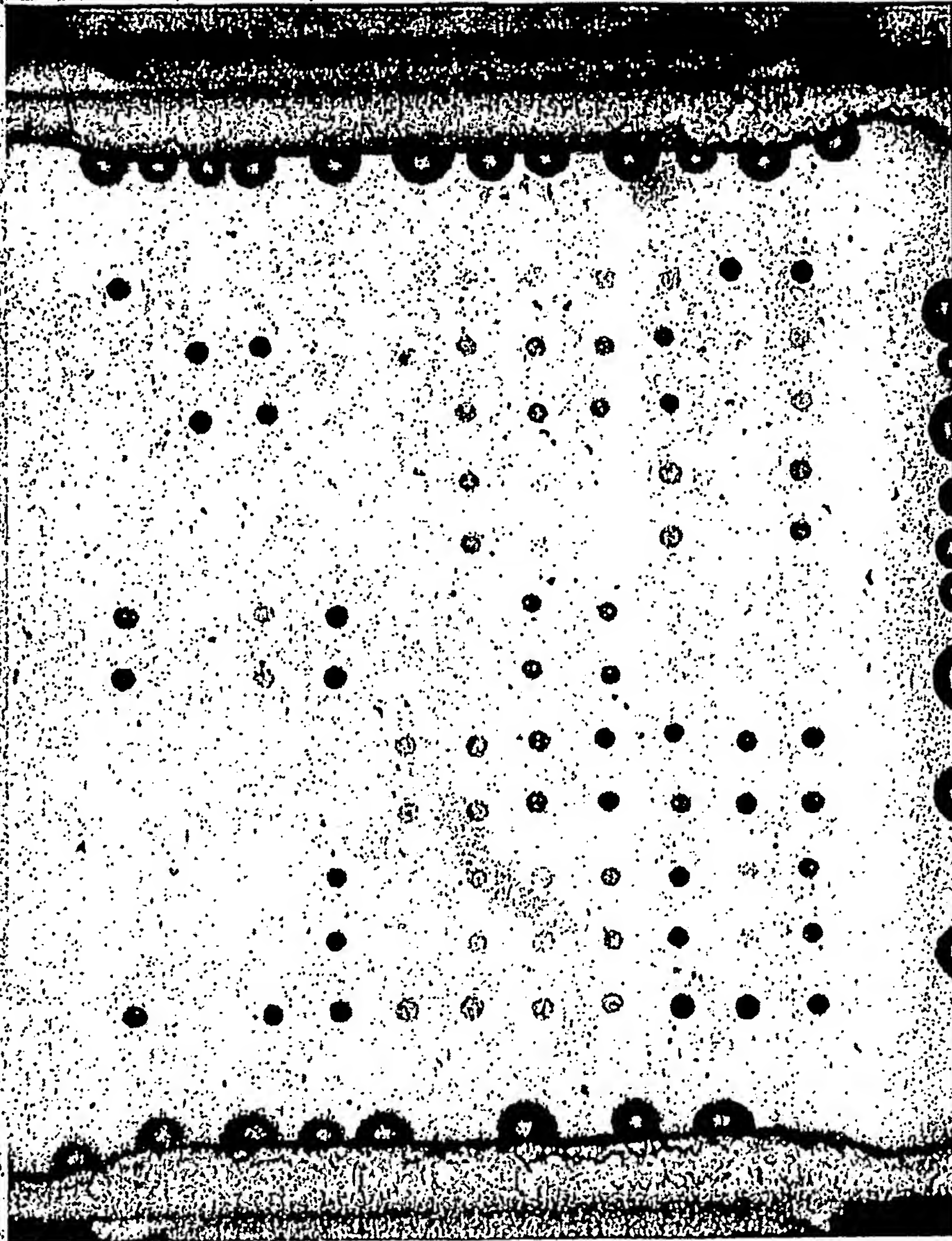
Fig.8

P. aeruginosa AT-Chip



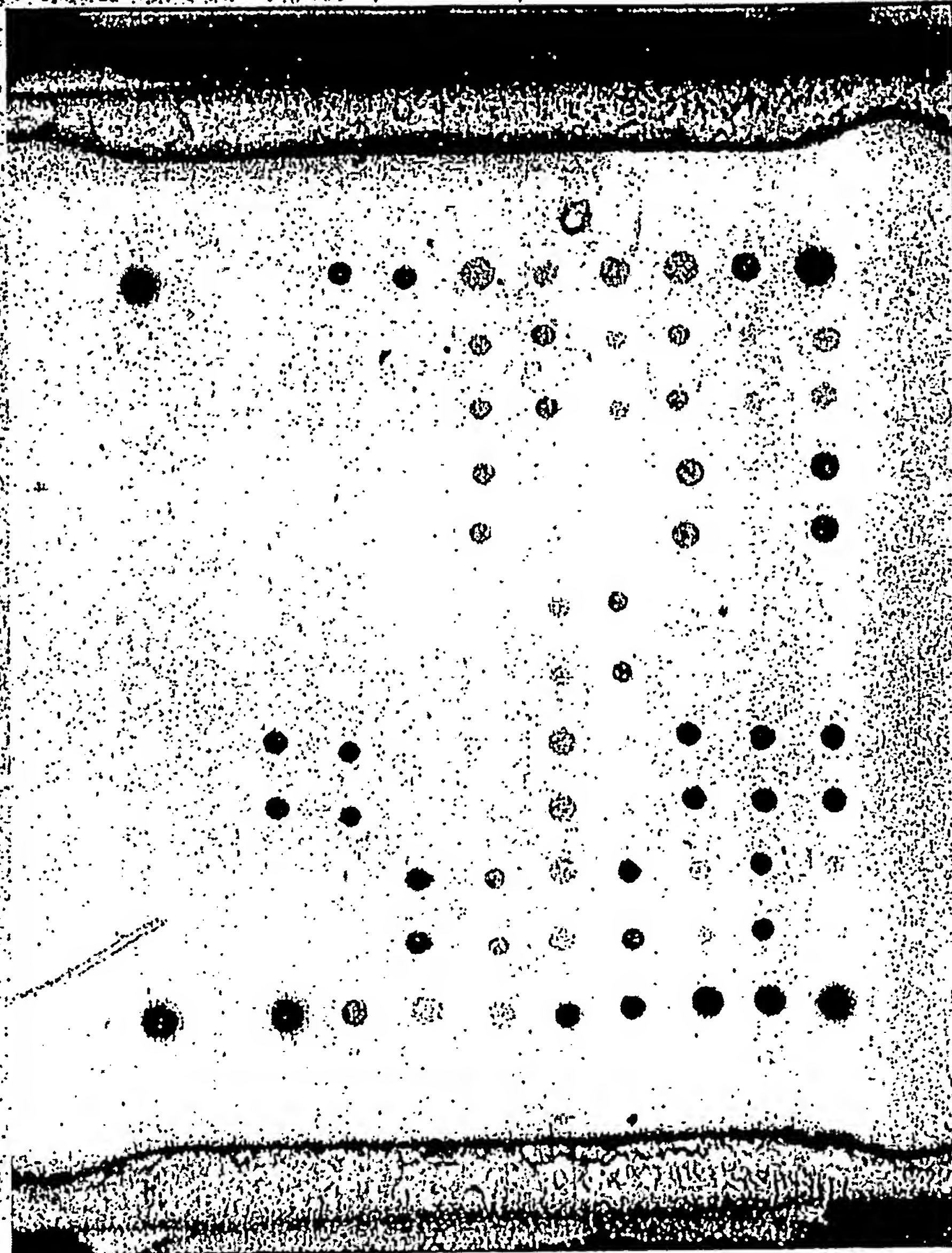
PT20

P. aeruginosa AT-Chip



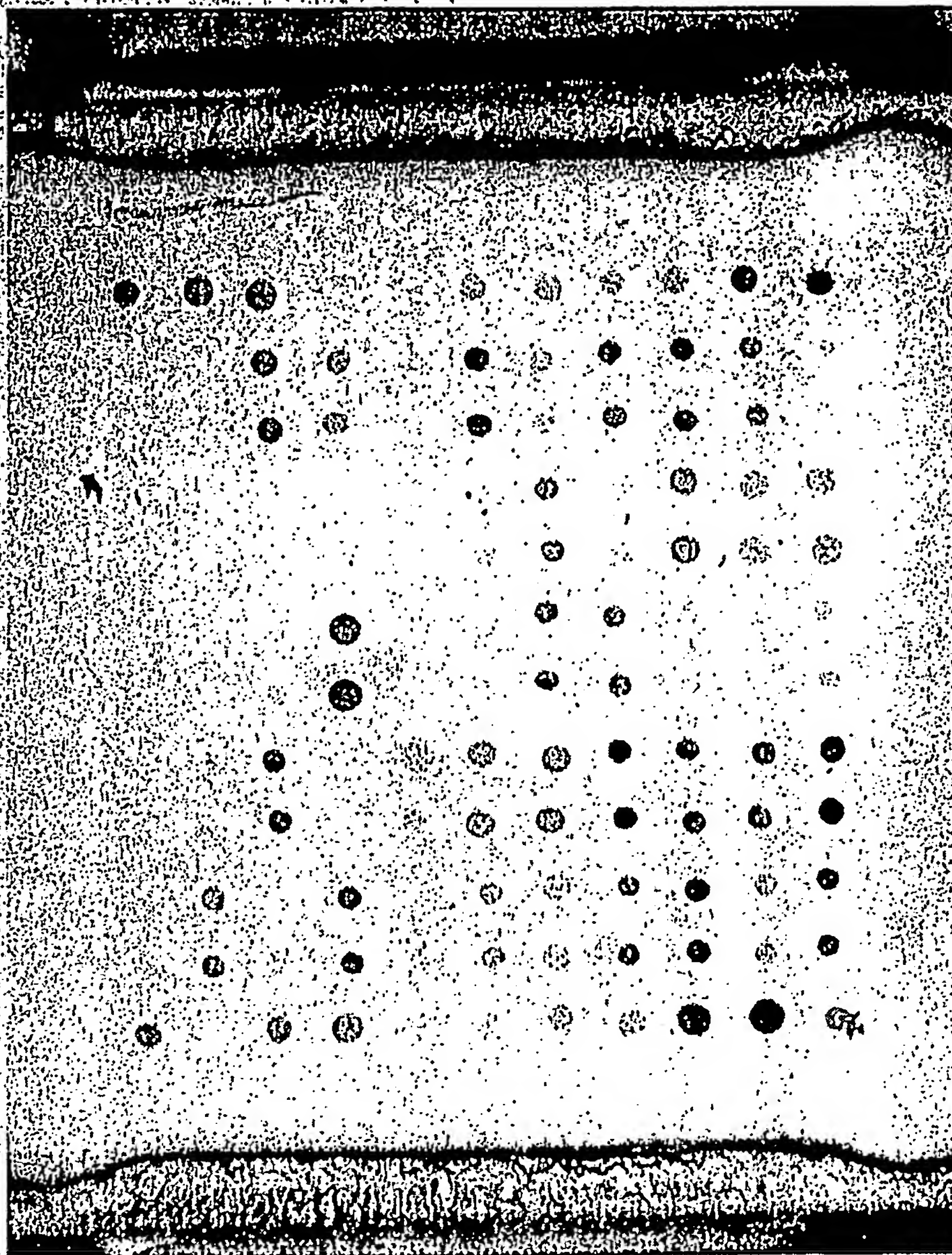
ZW79

P. aeruginosa AT-Chip



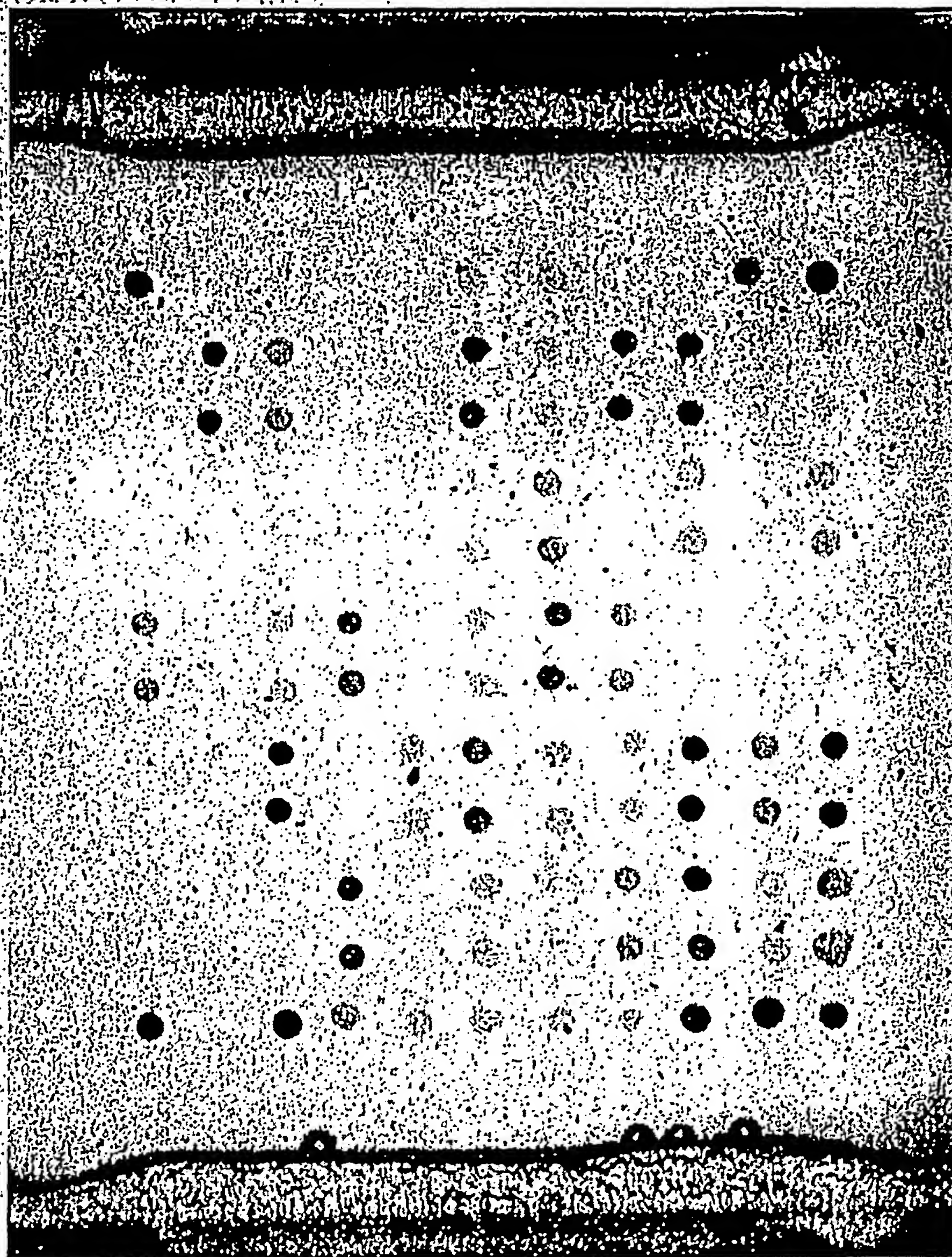
ZW85

P. aeruginosa AT-Chip



2813A

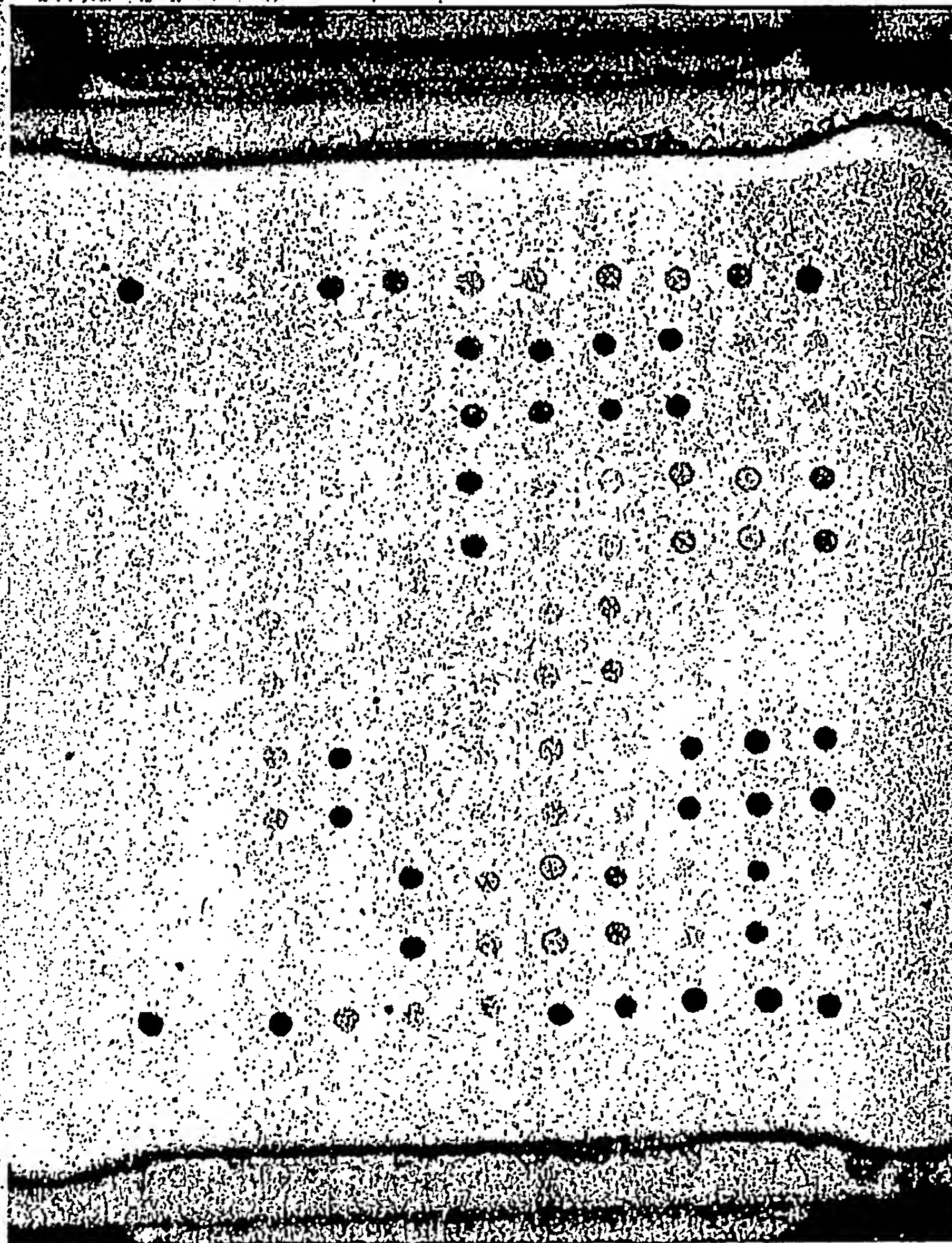
P. aeruginosa AT-Chip



KB1-85

Fig.13

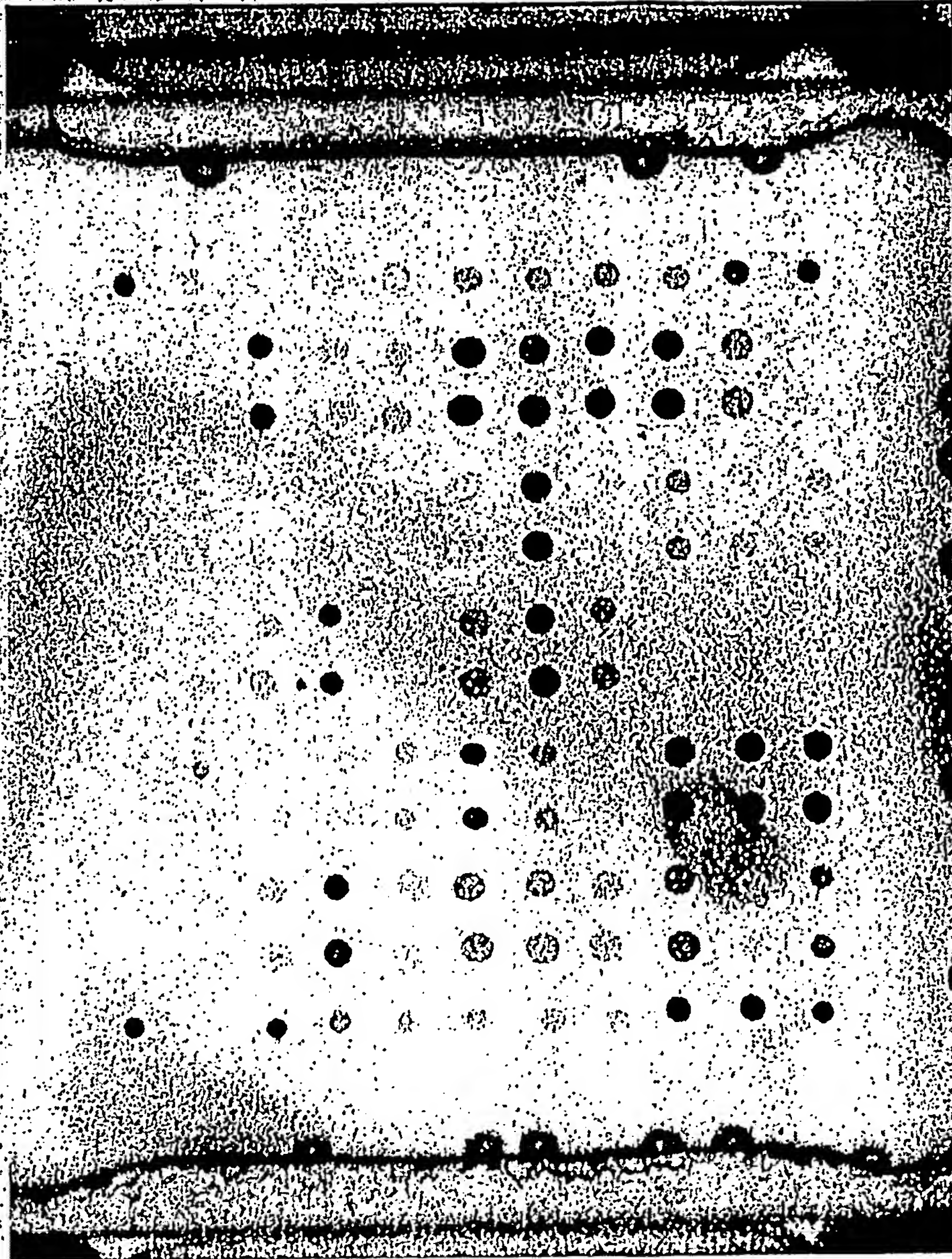
P. aeruginosa AT-Chip



ZW98

Fig.14

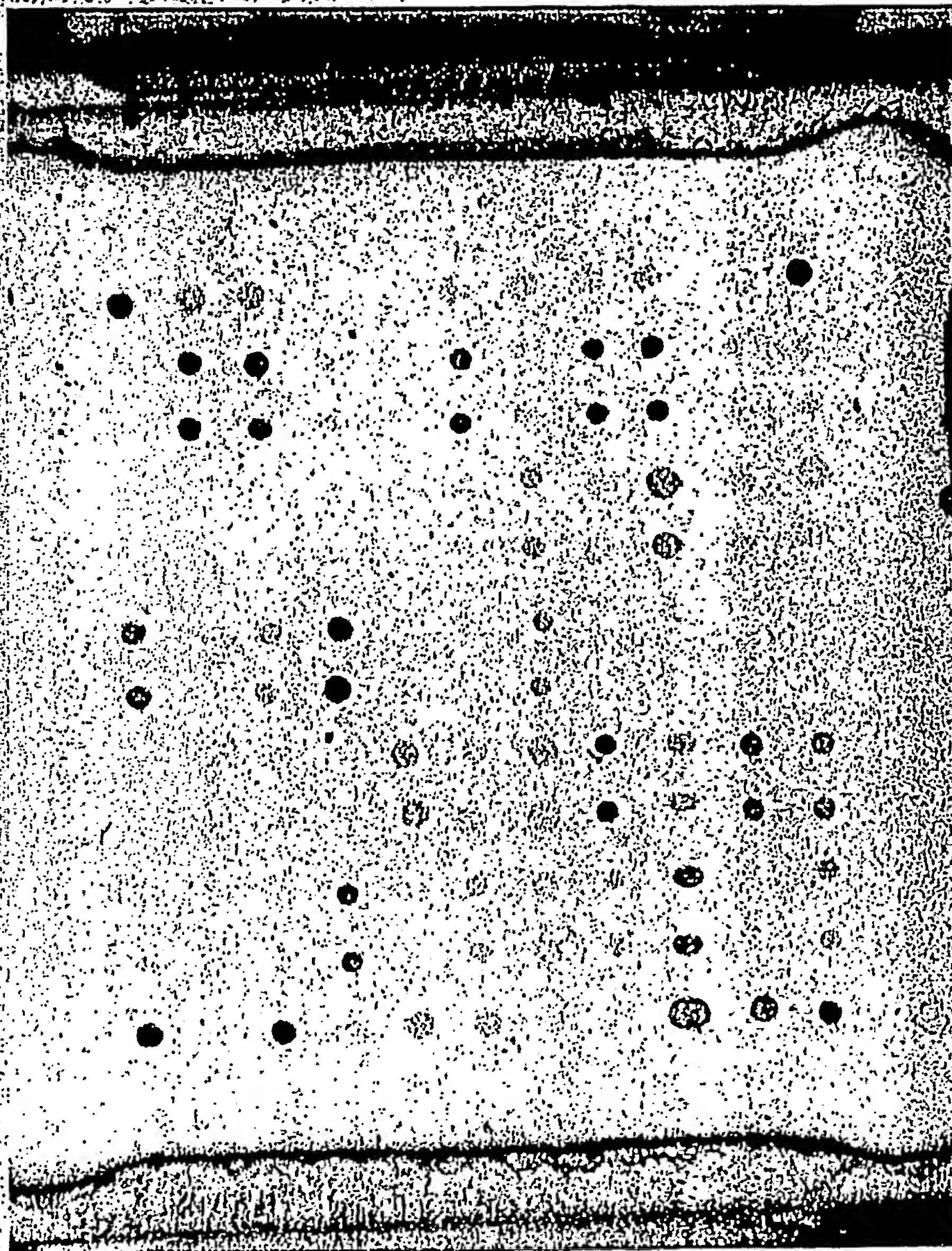
P. aeruginosa AT-Chip



641HD

Fig.15

P. aeruginosa AT-Chip



ATCC15522

Fig.16

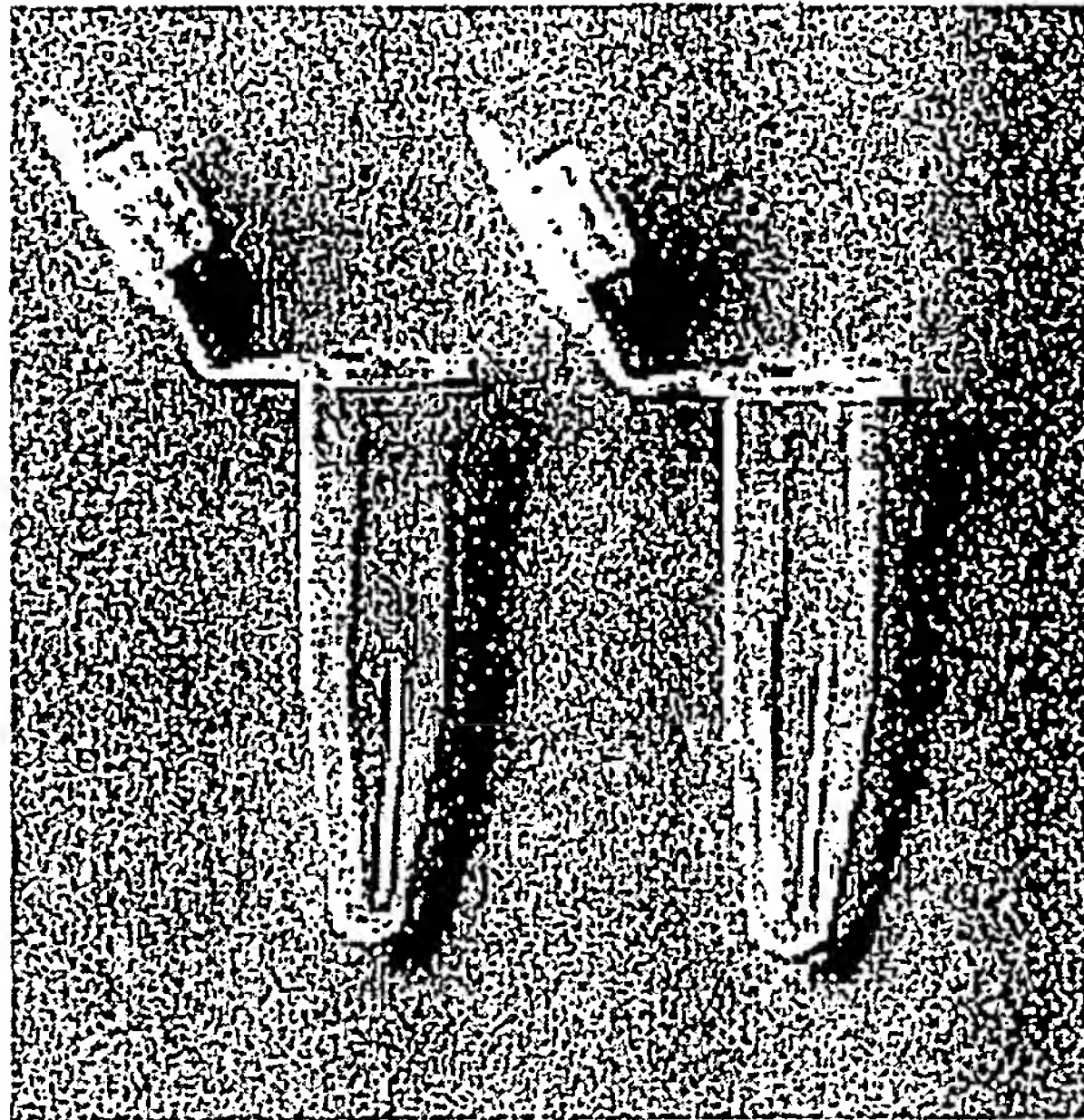


Fig.17a

47-1/23
ACGCGGATGTCCTGGATTG

47-1/39
CTGAAGAAGGGGCGCTACGCG

47-2/22
GCGTACCGGGCAAGGTGATAG

47-2/52
CTCGGTGAAACATCGGGAGGG

C45/18
TCATCCAGCAAGCCATTGCGC

C45/60a
GGAGTCGCTTCCGCCATCG

C45/60b
TGGAGTCGCTTCCGCCATCG

C46/15
AAGGGCGTTTCACGCTGACGC

C46/22
ATCCGGAAGGGCGTTTCACG

C46/88
TCCACACCTCAGACTTCGGCG

C47-1/43
TATTGACGACCTACCGCGCGC

C47-2/56a
GCAACTGATGTTGCCCCAGC

C47-2/56b
CGCAACTGATGTTGCCCCAGC

C47-2/59
ACACGCAACTGATGTTGCCCC

CIS-4/36
TGTCCCGGCTCAGTTCAACG

CIS-4/50
AACACCTTGGCGTTGTCCC

CIS-4/51
GCAACACCTTGGCGTTGTCC

CIS-5/4
TCAAGCTCGTTGTGGACCGC

CIS-5/48
GTTACGACGGCGTGCTGTCGG

CSP-1/39a
ACGCAACGTATTCGGCGACCC

CSP-1/39b
CGCAACGTATTCGGCGACCC

Fig.17b

fliAT/28
AGCTGATGGTATCGCCGTCGC

fliAT/72
CTAGTGATCGCACCGGAGCC

oriC/20
AGCCTCGACACCGGTTCTCG

oriC/54
TCGTTCATCCCCAGGCTTCG

oriC/59
ACCATCTCGTTCATCCCCAGG

oprL/53
TTCTGAGCCCAGGACTGCTCG

oprL/65
TCGACGCGACGGTTCTGAGCC

fliCb/36
TGACGTTCTCGCCGGTAGCG

fliCb/65
CAGTAGCGGTACCGGTCTGCG

fliCb/66
CAGTAGCGGTACCGGTCTGC

alkAG/27
TTCCTCGCCGGCATAGTAGGC

alkGA/32

alkGA/51
CGAGGACGAGGCATCTTCCGG

citAG/4
GCAGGTAGCAGGTTTCCAGG

citAG/46
AACTGTTCCCTTCTGCGCGGCG

citGC/8
TGATCGGCTTGGTCTCGCAGG

citGC/11
GCTGATCGGCTTGGTCTCGC

citGC/75
GAGGCGTTCTGCTCGTGGTCG

oprI/12
TTTTTCCAGCATGCGCAGGG

oprI/17
GCTGGCTTTTTCCAGCATGCG

oprI/22
TTGCGGCTGGCTTTTTCCAGC

Fig.17c

am7CA/1
TTGGGATAGTTGCGGTGGC

am7CA/27
CGTAGGCGATCTTCACCCGC

am7CA/29
TGGCGTAGGCGATCTTCACCC

am3CT/21
GGCGAGATAGCCGAACAGGC

am3CT/22
GCGGCGAGATAGCCGAACAGG

am3CT/69
CACTTGCTGCTCCATGAGCC

am2CT/35
GAGGTCGAGCAGGCTGATGC

am2CT/42
TAGGTCGCGAGGTCGAGCAGG

am2CT/92
GTCCTTCTGCACCGAGTCGG

am1GA/49
CGCATCTTGTCTGGGTCAGG

am1GA/58
TCGTCGAGGCGCATCTTGTCC

am45/1
ACGTCGAGGTGGGTCTGTTCCG

am45/96
GTAGCCTTCGGCATCCAGCG

am6TC/60
TCGGCATTGGGATAGTTGCGG

GI11/15
CCTCCTGTCTCATGCCGATGC

GI11/59
GCATTGCGCCACGGAAGGAAGG

GI11/71
GAAGGCATCATGGCATTGCGCC

GI18/62
GTCATGGGGTTTCCCAGAGACC

fliCa/41
GATCGCGATGTCGACGGTGCC

fliCa/42
CGATCGCGATGTCGACGGTGC

fliCa/46
TGCCGATCGCGATGTCGACG

Fig.17d

SG-1/40
GACGAATACCCAGCTGCGTGG

SG-1/43
GCAGACGAATACCCAGCTGCG

SG-4/1
CGCGACGTCGTGACGTCAGC

SG-4/67
ACTTTCGGCTCTTCGGGCTGG

TB46/21
AGGTAGAGACTCGGGGGAACC

TB46/45
TCGTTTTTCGGTCATGGCCAGG

TB471/22
TTCCGCGACGAACATCCGTGG

TB471/25
CGCTTCCGCGACGAACATCCG

TB472/36
GGATCGCTTCCGATAGGGCAGC

TB472/84
AGAGGCATGGGTCTGTACCG

TB473/34
TCTGTCAATCCCCTTTGGGG

TB473/41
AGCCCCTTTCTGTCAATCCCC

TB474/36
GGCTTCCTACCGAAGGTCAGG

TB474/41
TGAGGGCTTCCTACCGAAGG

exoS/31
TTCAAGGTCATGGGCAATGCC

exoS/37
AGTCCCTTCAAGGTCATGGGC

exoU/22
GCCGACTGAGCTGTAGCTCGG

exoU/23
GGCCGACTGAGCTGTAGCTCG

exoU/42
ACCAGACTGGTCAATGGTGG

flins/2
CCCGTGTTCGGTAGACCTTGC

pKL11/49a
AGCAGTTACCCACAGCATGG

Fig.17e

pKL11/49b
CAGCAGTTACCCACAGCATGG

pKL3/47
CTACACTCCAACCGCTGGTCC

pKL3/50
GACCTACACTCCAACCGCTGG

pKL3/80
TTCCCTTGCTGCCGAGAAGC

pKL7/14
TAATAGGCGAGCCTGCCGTCC

47D7nw1a
TCCACGCCGAGGGACGTGCC

47D7nw1b
GCTCCACGCCGAGGGACGTGCC

C46-nw1a
CGCGGTGCTGGTTGCGCTGC

C46-nw1b
CCAATGCCCAGGGCCAGCGGA

C46-nw1c
CGCTGGCAGTTCCGCTGGCC

ExoSnw1a
CAGGGTCGCCAGCTCGCTCGCC

ExoSnw1b
AGGGTCGCCAGCTCGCTCGC

ExoUnw1a
AGTGATCTGCCGCGGCCCTGCC

ExoUnw1b
GTGATCTGCCGCGGCCCTGC

OrfA-1
GTTCCACAGGCGCTGCGGCGC

OrfA-2
GTTCCACAGGCGCTGCGGCG

OrfA-3
CAAAGCCCCTGGTCGCGCGG

OrfC-1
GCAGCTTTTCCACCGCCGGCGG

OrfI-1
AAACTGCCCCGCCCCCATCC

OrfI-2
GGAAAACTGCCCCGCCCCC

OrfJ-1
ACGCTCGCAGCGCCTCACGCG

OrfJ-2
GGCCTGGCTGCGAACGCTCGC

Fig.17f

no	tube	name	5'-3'-sequence	group	length	GC-content [%]	Tm [°C]	spot-ID's
1	Pa-S_001	oriC T-C_wt	GAAGCCGAGCAATTGCGTGTTC	1	23	52,2	62,4	14,15
2	Pa-S_056	oriC T-C_mut_1	GAAGCCGAGCAACTGCGTGTTC	1	23	56,5	64,2	4,5
3	Pa-S_057	oprL T-C_wt_1	GGTGCTGCAGGGTGTTCGCCGG	1	23	69,6	69,6	16,17
4	Pa-S_058	oprL T-C_mut_1	GGTGCTGCAGGGCGTTTCGCCGG	1	23	73,9	71,3	6,7
5	Pa-S_059	fliC a A-T_wt_1	CAAGATCGCCGCGAGCGGTCAAC	1	22	63,6	65,8	18,19
6	Pa-S_060	fliC a A-T_mut_1	CAAGATCGCCGCGTGGTCAAC	1	22	63,6	65,8	8,9
7	Pa-S_061	alkB2 G-A_wt_1	TGCTGCTGGCGCGGTGTGCTAT	1	23	65,2	67,8	20,21
8	Pa-S_062	alkB2 G-A_mut_1	TGCTGCTGGCAGCGGTGTGCTAT	1	23	60,9	66,0	10,11
9	Pa-S_063	alkB2 A-G_wt_1	CCTCGCCCTGTTCCTCCACCGCTCTGG	1	25	72,0	72,8	22,23
10	Pa-S_064	alkB2 A-G_mut_1	CTCGCCCTGTTCCTCCGCGCTCTGG	1	24	75,0	73,0	26,27
11	Pa-S_065	ciIS A-G_wt_1	TCGAGCAACTGGCAGAGAAATCCG	1	24	54,2	64,4	38,39
12	Pa-S_066	ciIS A-G_mut_1	CGAGCAACTGGCGGAGAAATCCG	1	23	60,9	66,0	28,29
13	Pa-S_067	ciIS G-C_wt_1	GCGGAAAACCTTCCTGCACATGATGTT	1	26	46,2	63,2	40,41
14	Pa-S_068	ciIS G-C_mut_1	GCGGAAAACCTTCCTCCACATGATGTT	1	26	46,2	63,2	30,31
15	Pa-S_069	oprI T-C_wt_1	AGCTCAGCAGACTGCTGACGAGG	1	23	60,9	66,0	42,43
16	Pa-S_070	oprI T-C_mut_1	AGCTCAGCAGACCGCTGACGAG	1	22	63,6	65,8	32,33
17	Pa-S_071	ampC_1 G-A_wt_1	AAGAGGACGGCGCGCGGTGACGCC	1	25	76,0	74,5	44,45
18	Pa-S_072	ampC_1 G-A_mut_1	AAGAGGACGGCGCGCGGTGACGCCG	1	26	73,1	74,3	34,35
19	Pa-S_019	ampC_2 C-T_wt	GACAAGATGCGCCTCGACGACC	1	22	63,6	65,8	46,47
20	Pa-S_073	ampC_2 C-T_mut_1	GACAAGATGCGTCTCGACGACCG	1	23	60,9	66,0	50,51
21	Pa-S_021	ampC_3 C-T_wt	AGCCGACCTACGCGCCCGGCAG	1	22	77,3	71,4	62,63
22	Pa-S_074	ampC_3 C-T_mut_1	CAGCCGACCTATGCGCCCGGCAG	1	23	73,9	71,3	52,53
23	Pa-S_075	ampC_4 G-A_wt_1	CCGTTCGAACGGCTCATGGAGCA	1	23	60,9	66,0	64,65
24	Pa-S_076	ampC_4 G-A_mut_1	GCCGTTCGAACGACTCATGGAGCA	1	24	58,3	66,1	54,55
25	Pa-S_077	ampC_5 G-C_wt_1	TGGAGCAGCAAGTGTCCCGGC	1	22	63,6	65,8	

Fig.18a

25	Pa-S_078	ampC_5 G-	TGGAGCAGCAACTGTTCCTGGC	1	22	63,6	65,8	66,67
27	Pa-S_027	ampC_6 T-C_wt	GAACAAGACCGGTTCCACCAACGG	1	24	58,3	66,1	56,57
28	Pa-S_079	ampC_6 T-	AACAAGACCGGCTCCACCAACGG	1	23	60,9	66,0	68,69
29	Pa-S_029	ampC_7 C-A_wt	GCGACCTGGGCTTGATCCT	1	22	68,2	67,7	58,59
30	Pa-S_080	ampC_7 C-	GCGACCTGGGACTGGTGATCCT	1	22	63,6	65,8	70,71
31	Pa-S_031	A_mut_1	GCCGACCAACTGAAGTCCAACTCG	2	24	58,3	66,1	74,75
32	Pa-S_032	fliC a	GTCGCIGAACGGCACCTACTTCA	2	23	56,5	64,2	86,87
33	Pa-S_033	exoS-1	CAGCCTGCGGTCAATGTCTCTCGG	3	22	68,2	67,7	76,77
34	Pa-S_034	exoU	CGCCAGTTTGAGAACGGAGTCACC	3	24	58,3	66,1	88,89
35	Pa-S_038	C-47-1	GCGGATCTTCTCCACTTCATCGG	4	24	54,2	64,4	78,79
36	Pa-S_039	C-47-2	GCCTCCGCGATTGAACATCGTGAT	4	24	58,3	66,1	90,91
37	Pa-S_040	47D7-1	GTAGCGGAGTCGAGCGGAATCAT	5	24	54,2	64,4	80,81
38	Pa-S_041	47D7-2	GTGAGCATGGATTCGGCAGTCGTT	5	24	58,3	66,1	92,93
39	Pa-S_054	C-45	CGAGGAGTTTCGGACCGGCTTGA	6	24	54,2	64,4	82,83
40	Pa-S_055	C-46	AATAGGACCGGCAGAACGGGCATT	6	24	58,3	66,1	94,95
41	Pa-S_035	C-inselspez-4	GCGCCTTCTCCTCTTTCGAGATGT	7	24	54,2	64,4	98,99
42	Pa-S_036	C-inselspez-5	CAGTATGGTACGGACACGAAGCCG	7	24	58,3	66,1	110,111
43	Pa-S_037	C-spezifisch-1	GCATCATTCGCGGTGACATCTGGT	8	24	58,3	66,1	122,123
44	Pa-S_044	pKL-3	TCTGAACCTGGGGCTATCACCTGGA	9	24	54,2	64,4	100,101
45	Pa-S_045	pKL-7	AATTGATGGCTTCTCAGGCGCAGG	9	24	54,2	64,4	112,113
46	Pa-S_046	pKL-11	AGTCATGGGACTGAATACGGCGACT	9	25	52,0	64,6	124,125
47	Pa-S_042	PAGI-1-1	TTCCTGGTGTGAGGATCTCGG	10	24	58,3	66,1	102,103
48	Pa-S_043	PAGI-1-8	TGGTAGCTCTCGACGTACTGGCTG	10	24	58,3	66,1	114,115
49	Pa-S_047	SG17M-1	CCCGTTGCTCATACCCGTTCTCTG	11	24	58,3	66,1	104,105
50	Pa-S_048	SG17M-4	AGGGCATTCCTCAGGTGGACTCAGG	11	24	54,2	64,4	116,117
51	Pa-S_053	fla-insel-1	ACCTGTGTGCGTGGAGGGTATGTT	12	24	58,3	66,1	106,107
52	Pa-S_049	TB-C47-1	AGCGTCCCTGACCAAGCTCATCAG	13	24	58,3	66,1	118,119
53	Pa-S_050	TB-C47-2	CGCCAAACAATTCCGCCATTACAGCG	13	24	54,2	64,4	126,127
54	Pa-S_051	TB-C47-3	TCCAACAGGCGAGGTACAGGGTG	13	24	58,3	66,1	128,129

Fig.18b

55	Pa-S_052	TB-C47-4	CGCTGCACATACAGGTCCGTTCTC	13	24	54,2	64,4	130,131
56	Biotin + Cy3-marker							
57	Pa-S_081	oriC T-C_wt_1	AGCCCCAGCAATTGCGTGTTTCTCCG	1	25	65,6	56	1,12,97,121,132
58	Pa-S_082	oriC T-C_mut_2	AGCCCCAGCAACTGCGTGTTTCTCC	1	24	65,1	58	
59	Pa-S_083	alkB2 G-A_wt_2	GCTGCTGGCGGCGGTGTGC		19	67,4	79	8,9
60	Pa-S_084	alkB2 G-A_mut_2	TGCTGCTGGCAGCGGTGTGCT		21	67,3	67	20,21
61	Pa-S_085	opr1 T-C_wt_2	CAGAAAGCTCAGCAGACTGCTGACGAG		27	64,6	56	
62	Pa-S_086	opr1 T-C_mut_2	GAAAGCTCAGCAGACCGCTGACGAG		25	64,9	60	
63	Pa-S_087	ampC_1 G-A_wt_2 ampC_1 G-	ACGGCCGCCGCGGTGACGCC		19	70,2	84	
64	Pa-S_088	A_mut_2	ACGGCCGCCCAGGTGACGCCG		20	69,9	80	
65	Pa-S_089	ampC_3 C-T_wt_1 ampC_3 C-	GCCGACCTACGCGCCGGGC		19	68,4	84	
66	Pa-S_090	T_mut_2	AGCCGACCTATGCGCCGGGCA		21	68,4	71	
67	Pa-S_091	ampC_4 G-A_wt_2 ampC_4 G-	GTTCGAACGGCTCATGGAGCAGCA		24	65	58	
68	Pa-S_092	A_mut_2	GTTCGAACGACTCATGGAGCAGCAAG		26	63,5	54	
69	Pa-S_093	exoS-1_1	CAGCCCAGTCAGGACGCGCA		20	64,9	70	
70	Pa-S_094	exoU_1	AGTGACGTGCGTTTCAGCAGTCCC		24	64,8	58	
71	Pa-S_095	47D7-1_1	GTGTCACGGCCCATGTCTAGCAGC		24	65	63	
72	Pa-S_096	C-46_1	CGAAGTCTGAGGTGTGGACCCGC		23	64,5	65	
73	Pa-S_097	Fla-Insel-2_orfA	CGCTGGAGGGTATGTTCGCGCAAGG		24	64,8	63	
74	Pa-S_098	Fla-Insel-2_orfC	CGTACTCAGCTTCTCCACCCAGCG		24	64,3	63	
75	Pa-S_099	Fla-Insel-2_orfI	CCTGGACCTCTCCAAGGTTCCCT		24	65	63	
76	Pa-S_100	Fla-Insel-2_orfJ	GCCATTCCGACGACCAACAAGGC		24	64,2	58	

group "mother"

Fig.18c

well- no	tube	name	5'-3'-sequence	group	length	GC- content [%]	Tm [°C]	spot- ID's
1	Pa-S_001	oriC T-C_wt	GAAGCCAGCAATTGCGTGTTC	1	23	52,2	62,4	23
2	Pa-S_056	oriC T-C_mut_1	GAAGCCAGCAACTGCGTGTTC	1	23	56,5	64,2	14,15
57	Pa-S_081	oriC T-C_wt_1	AGCCAGCAATTGCGTGTTC	1	25	65,6	56	13,25
58	Pa-S_082	oriC T-C_mut_2	AGCCAGCAACTGCGTGTTC	1	24	65,1	58	37,49
3	Pa-S_057	oprL T-C_wt_1	GGTGCTGCAGGGTGTTCGCCGG	1	23	69,6	69,6	4,5
4	Pa-S_058	oprL T-C_mut_1	GGTGCTGCAGGGGTTCGCCGG	1	23	73,9	71,3	16,17
5	Pa-S_059	fliC a A-T_wt_1	CAGATCGCCGCGAGCGGTCAAC	1	22	63,6	65,8	6,7
6	Pa-S_060	fliC a A-T_mut_1	CAGATCGCCGCGTGGGTCAAC	1	22	63,6	65,8	18,19
59	Pa-S_083	alkB2 G-A_wt_2	GCTGCTGGCGGGGTGTGC	1	19	67,4	79	8,9
60	Pa-S_084	alkB2 G-A_mut_2	TGCTGCTGGCAGCGGTGTGCT	1	21	67,3	67	20,21
9	Pa-S_063	alkB2 A-G_wt_1	CCTCGCCCTGTTCACCGCTCTGG	1	25	72,0	72,8	10,11
10	Pa-S_064	alkB2 A-G_mut_1	CTCGCCCTGTTCGCCCGCTCTGG	1	24	75,0	73,0	22,23
11	Pa-S_065	citS A-G_wt_1	TCGAGCAACTGGCAGAGAAATCCG	1	24	54,2	64,4	26,27
12	Pa-S_066	citS A-G_mut_1	CGAGCAACTGGCGGAGAAATCCG	1	23	60,9	66,0	38,39
13	Pa-S_067	citS G-C_wt_1	GCGGAAAACCTTCCTGCACATGATGT	1	26	46,2	63,2	28,29
14	Pa-S_068	citS G-C_mut_1	GCGGAAAACCTTCCTCCACATGATGT	1	26	46,2	63,2	40,41
15	Pa-S_039	oprL T-C_wt_1	AGCTCAGCAGACTGCTGACGAGG	1	23	60,9	66,0	30,31
16	Pa-S_070	oprL T-C_mut_1	AGCTCAGCAGACCGCTGACGAG	1	22	63,6	65,8	42,43
61	Pa-S_085	oprL T-C_wt_2	CAGAAAGCTCAGCAGACTGCTGACGAG	1	27	64,6	56	61,73
62	Pa-S_086	oprL T-C_mut_2	GAAAGCTCAGCAGACCGCTGACGAG	1	25	64,9	60	24,85
63	Pa-S_087	ampC_1 G-A_wt_2 ampC_1 G-	ACGGCCGCCGGGTGACGCC	1	19	70,2	84	32,33
64	Pa-S_088	A_mut_2	ACGGCCGCCAGGTGACGCCG	1	20	69,9	80	44,45
19	Pa-S_019	ampC_2 C-T_wt ampC_2 C-	GACAAAGATGCGCCTCGACGACC	1	22	63,6	65,8	34,35
20	Pa-S_073	T_mut_1	GACAAAGATGCGTCTCGACGACCG	1	23	60,9	66,0	46,47
21	Pa-S_021	ampC_3 C-T_wt ampC_3 C-	AGCCGACCTACGCGCCGGGCAG	1	22	77,3	71,4	50,51
22	Pa-S_074	T_mut_1	CAGCCGACCTATGCGCCGGGCAG	1	23	73,9	71,3	62,63

Fig.19a

65	Pa-S_089	ampC_3 C-T_wt_1	GCCGACCTACGCCCGGGC	1	19	68,4	84	36,48
66	Pa-S_090	ampC_3 C-T_mut_2	AGCCGACCTATGCGCGGGCA	1	21	68,4	71	60,72
67	Pa-S_091	ampC_4 G-A_wt_2	GTTCCGAACGGCTCATGGAGCAGCA	1	24	65	58	52,53
68	Pa-S_092	ampC_4 G-A_mut_2	GTTCCGAACGACTCATGGAGCAGCAAG	1	26	63,5	54	64,65
25	Pa-S_077	ampC_5 G-C_wt_1	TGGAGCAGCAAGTGTTCCTCCGGC	1	22	63,6	65,8	54,55
26	Pa-S_078	ampC_5 G-C_mut_1	TGGAGCAGCAACTGTTCCTCCGGC	1	22	63,6	65,8	66,67
27	Pa-S_027	ampC_6 T-C_wt	GAACAAGACCGGTTCCACCAACGG	1	24	58,3	66,1	56,57
28	Pa-S_079	ampC_6 T-C_mut_1	AACAAGACCGGCTCCACCAACGG	1	23	60,9	66,0	68,69
29	Pa-S_029	ampC_7 C-A_wt	GCGACCTGGGCTTGGTGATCCT	1	22	68,2	67,7	58,59
30	Pa-S_080	ampC_7 C-A_mut_1	GCGACCTGGGACTGGTGATCCT	1	22	63,6	65,8	70,71
31	Pa-S_031	flhC b	GCCGACCACTGAACTCCAACTGG	2	24	58,3	66,1	74,75
32	Pa-S_032	flhC a	GTCGCTGAACGGCACCTACTTCA	2	23	56,5	64,2	86,87
69	Pa-S_093	exoS-1_1	CAGCCAGTCAGGACGGGCA	3	20	64,9	70	76,77
34	Pa-S_034	exoU	CGCCAGTTTGAGAACGGAGTCACC	3	24	58,3	66,1	88,89
70	Pa-S_094	exoU_1	AGTGACGTGGGTTTCAGCAGTCCC	3	24	64,8	58	84,96
35	Pa-S_038	C-47-1	GCGGGATCTTGTGCACTTCATGGG	4	24	54,2	64,4	78,79
71	Pa-S_035	47D7-1_1	GTGTCACGGCCCATGTCAGCAGC	5	24	65,2	63	80,81
38	Pa-S_041	47D7-2	GTGAGCATGGAATCGGCAGTCGTT	5	24	58,3	66,1	92,93
39	Pa-S_054	C-45	CGAGGAGTTTCGGACCGGCTTTGA	6	24	54,2	64,4	82,83
40	Pa-S_055	C-46	AATAGGACCGGCAGAACGGGCATT	6	24	58,3	66,1	94,95
72	Pa-S_056	C-46_1	CGAAGTCTGAGGTGTGGACCCGC	6	23	64,5	65	108,120
41	Pa-S_035	C-Inselspez.-4	GCGCCTTCTCCTCTTTCAGATGT	7	24	54,2	64,4	98,99
42	Pa-S_036	C-Inselspez.-5	CAGTATGGTACGGACACGAAGCGC	7	24	58,3	66,1	110,111
43	Pa-S_037	C-spezifisch-1	GCATCATGCGCGTCAGATCTGGT	8	24	58,3	66,1	122,123
44	Pa-S_044	pKL-3	TCTGAACCTGCGGCTATCACCTGGA	9	24	54,2	64,4	100,101
46	Pa-S_046	pKL-11	AGTCATGGGACTGAATACGGCGACT	9	25	52,0	64,6	124,125
47	Pa-S_042	PAGI-1-1	TTCTCGGTGTCGAGGATCTCGG	10	24	58,3	66,1	102,103
48	Pa-S_043	PAGI-1-8	TGGTAGCTCTCGACGTACTGGCTG	10	24	58,3	66,1	114,115

Fig.19b

49	Pa-S_047	SG17M-1	CCCGTTGCTCATAAACCGTTCCTG	11	24	58,3,66,1	104,105
50	Pa-S_048	SG17M-4	AGGGCATTCTCAGGTGGACTCAGG	11	24	54,2	64,4 116,117
51	Pa-S_053	fla-insel-1	ACCTGTGTGGCTGGAGGTATGTT	12	24	58,3,66,1	106,107
54	Pa-S_051	TB-C47-3	TCCAACAGGCAGGAGTACAGGGTG	13	24	58,3,66,1	128,129
55	Pa-S_052	TB-C47-4	CGCTGCACATACAGGTCCGTTCTC	13	24	54,2	64,4 130,131
73	Pa-S_097	Fla-Insel-2_orfA	CGCTGGAGGGTATGTTCGGCAAGG	14	24	64,8	63 90,91
74	Pa-S_098	Fla-Insel-2_orfC	CGTACTCAGCTTCTCCACCCAGCG	14	24	64,3	63 112,113
75	Pa-S_099	Fla-Insel-2_orfI	CCTGGACCTCTCCAAGGTTCCGCT	14	24	65	63 118,119
76	Pa-S_100	Fla-Insel-2_orfJ	GCCATTCCGACGACCAACAAGGC	14	24	64,2	58 126,127
56	Biotin + Cy3-marker						1,12,97,121,132
	group "mother"						

Fig.19c

Fig.20

Chip: MHH_P_aer_array2 (12x11 array with spot distance of 19.00 mm)

56	43	43	46	46	76	76	54	54	55	55	56
	42	42	74	74	48	48	50	50	75	75	72
56	41	41	44	44	47	47	49	49	51	51	72
62	32	32	34	34	73	73	38	38	40	40	70
61	31	31	69	69	35	35	71	71	39	39	70
61	22	22	68	68	26	26	28	28	30	30	66
58	21	21	67	67	25	25	27	27	29	29	66
58	12	12	14	14	16	16	64	64	20	20	65
57	11	11	13	13	15	15	63	63	19	19	65
57	2	2	4	4	6	6	60	60	10	10	62
56	1	1	3	3	5	5	59	59	9	9	56

Fig.21

Chip occupancy

marker spot	C-spezifisch-1	pKL-11	Fla-Insel-2 orfJ	TB-C47-3	TB-C47-4	marker spot
mut_2 oprI T-C wt_2 oprI T-C wt_2	C-Insel-spezifisch-5	Fla-Insel-2 orfC	PAGI-1-8	SG17M-4	Fla-Insel-2 orfI	C-46_1
		pKL-3			fla-Insel-1	
marker spot	C-Insel-spezifisch-4		PAGI-1-1	SG17M-1		C-46_1
mut_2 oprI T-C wt_2 oprI T-C wt_2	flic A	exoU	Fla-Insel-2 orfA	47D7-2	C-46	exoU_1
		exoS-1_1				
			C-47-1	47D7-1_1	C-45	exoU_1
mut_2 oriC T-C mut_2 oriC T-C wt_1 oriC T-C wt_1	mut_1 ampC_3 C-T wt	mut_2 ampC_4 G-A wt_2	mut_1 ampC_5 G-C wt_1	mut_1 ampC_6 T-C wt	mut_1 ampC_7 C-A wt	mut_2 ampC_3 C-T mut_2 ampC_3 C-T wt_1 ampC_3 C-T wt_1
		mut_1 citS A-G wt_1	mut_1 oprI T-C wt_1	mut_2 ampC_1 G-A wt_2	mut_1 ampC_2 C-T wt	
marker spot	mut_1 oriC T-C wt	mut_1 oprL T-C wt_1	mut_1 fliC a A-T wt_1	mut_2 alkB2 G-A wt_2	mut_1 alkB2 A-G wt_1	oprI T-C mut_2 marker spot